

# SEQUENCE LISTING

<110> Degussa-Hüls AG

<120> Novel nucleotide sequences coding for the poxB gene

<130> 990159 BT

<140>

<141>

<160> 3

<170> PatentIn Ver. 2.1

<210> 1

<211> 2160

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (327)..(2063)

<220>

<221> -35\_signal

<222> (227)..(232)

<220>

<221> -10\_signal

<222> (256)..(261)

<400> 1

ttagaggcga ttctgtgagg tcactttttg tggggctcggg gtctaaattt ggccagtttt 60

cgaggcgacc agacaggcgt gcccacgatg tttaaataagg cgatcgggtg gcacatctgtgt 120

ttgggtttcga cgggctgaaa ccaaaccaga ctgcccagca acgacggaaa tcccaaaagt 180

gggcatccct gtttggtacc gaggatccac ccgggcctga aactccctgg caggcggggcg 240

aagcgtggca acaactggaa tttaagagca caattgaagt cgcaccaagt taggcaaacac 300

aatagccata acgttgagga gttcag atg gca cac agc tac gca gaa caa tta 353

Met Ala His Ser Tyr Ala Glu Gln Leu

1

5

att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 401

Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val

10

15

20

25

ggg gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att 449

Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile

30

35

40

gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt 497

Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly

45

50

55

gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt 545

Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys

60	65	70	
ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg 75 80 85			593
aat ggt gcg aag gtg ttg gcc atc gct agc cat att ccg agt gcc cag Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln 90 95 100 105			641
att ggt tcg acg ttc ttc cag gaa acg cat ccg gag att ttg ttt aag Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys 110 115 120			689
gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt gag cag ggt gaa Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu 125 130 135			737
cgc att ttg cat cac gcg att cag tcc acc atg gcg ggt aaa ggt gtg Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val 140 145 150			785
tcg gtg gta gtg att cct ggt gat atc gct aag gaa gac gca ggt gac Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu Asp Ala Gly Asp 155 160 165			833
ggt act tat tcc aat tcc act att tct tct ggc act cct gtg gtg ttc Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr Pro Val Val Phe 170 175 180 185			881
ccg gat cct act gag gct gca gcg ctg gtg gag gcg att aac aac gct Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala Ile Asn Asn Ala 190 195 200			929
aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag aat gct cgc gcg Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys Asn Ala Arg Ala 205 210 215			977
cag gtg ttg gag ttg gcg gag aag att aaa tca ccg atc ggg cat gcg Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro Ile Gly His Ala 220 225 230			1025
ctg ggt ggt aag cag tac atc cag cat gag aat ccg ttt gag gtc ggc Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro Phe Glu Val Gly 235 240 245			1073
atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat gcg tcc aat gag Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp Ala Ser Asn Glu 250 255 260 265			1121
gcg gat ctg ctg att cta ttg ggt acg gat ttc cct tat tct gat ttc Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro Tyr Ser Asp Phe 270 275 280			1169
ctt cct aaa gac aac gtt gcc cag gtg gat atc aac ggt gcg cac att Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn Gly Ala His Ile 285 290 295			1217
ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt gat gtt gct gca Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly Asp Val Ala Ala 300 305 310			1265

aca atc gaa aat att ttg cct cat gtg aag gaa aaa aca gat cgt tcc	1313
Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys Thr Asp Arg Ser	
315 320 325	
ttc ctt gat cgg atg ctc aag gca cac gag cgt aag ttg agc tcg gtg	1361
Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys Leu Ser Ser Val	
330 335 340 345	
gta gag acg tac aca cat aac gtc gag aag cat gtg cct att cac cct	1409
Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val Pro Ile His Pro	
350 355 360	
gaa tac gtt gcc tct att ttg aac gag ctg gcg gat aag gat gcg gtg	1457
Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp Lys Asp Ala Val	
365 370 375	
ttt act gtg gat acc ggc atg tgc aat gtg tgg cat gcg agg tac atc	1505
Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His Ala Arg Tyr Ile	
380 385 390	
gag aat ccg gag gga acg cgc gac ttt gtg ggt tca ttc cgc cac ggc	1553
Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser Phe Arg His Gly	
395 400 405	
acg atg gct aat gcg ttg cct cat gcg att ggt gcg caa agt gtt gat	1601
Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala Gln Ser Val Asp	
410 415 420 425	
cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt ggt ttg ggc atg	1649
Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly Gly Leu Gly Met	
430 435 440	
ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa ctt ccg ctg aag	1697
Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln Leu Pro Leu Lys	
445 450 455	
gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg aag ttg gag atg	1745
Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val Lys Leu Glu Met	
460 465 470	
ctc gtg gag gga cag cca gaa ttt ggt act gac cat gag gaa gtg aat	1793
Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His Glu Glu Val Asn	
475 480 485	
ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg gta cgc atc acc	1841
Phe Ala Glu Ile Ala Ala Ala Ala Gly Ile Lys Ser Val Arg Ile Thr	
490 495 500 505	
gat ccg aag aaa gtt cgc gag cag cta gct gag gca ttg gca tat cct	1889
Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala Leu Ala Tyr Pro	
510 515 520	

gga cct gta ctg atc gat atc gtc acg gat cct aat gcg ctg tcg atc 1937  
 Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn Ala Leu Ser Ile  
                   525                                  530                                  535

cca cca acc atc acg tgg gaa cag gtc atg gga ttc agc aag gcg gcc 1985  
 Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe Ser Lys Ala Ala  
                   540                                  545                                  550

acc cga acc gtc ttt ggt gga gga gta gga gcg atg atc gat ctg gcc 2033  
 Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met Ile Asp Leu Ala  
                   555                                  560                                  565

cgt tcg aac ata agg aat att cct act cca tgatgattga tacacctgct 2083  
 Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro  
 570                                  575

gtttctcattg accgcgagcg cttaactgcc aacatttcca ggatggcagc tcacgccggt 2143

gccccatgaga ttgcctt 2160

<210> 2  
 <211> 579  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 2  
 Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln  
   1                                  5                                  10                                  15

Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile  
                   20                                  25                                  30

Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn  
                   35                                  40                                  45

Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly  
                   50                                  55                                  60

Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu  
   65                                  70                                  75                                  80

Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala  
                   85                                  90                                  95

Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln  
                   100                                  105                                  110

Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu  
                   115                                  120                                  125

Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile  
   130                                  135                                  140

Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly  
   145                                  150                                  155                                  160

Asp	Ile	Ala	Lys	Glu	Asp	Ala	Gly	Asp	Gly	Thr	Tyr	Ser	Asn	Ser	Thr	165	170	175
Ile	Ser	Ser	Gly	Thr	Pro	Val	Val	Phe	Pro	Asp	Pro	Thr	Glu	Ala	Ala	180	185	190
Ala	Leu	Val	Glu	Ala	Ile	Asn	Asn	Ala	Lys	Ser	Val	Thr	Leu	Phe	Cys	195	200	205
Gly	Ala	Gly	Val	Lys	Asn	Ala	Arg	Ala	Gln	Val	Leu	Glu	Leu	Ala	Glu	210	215	220
Lys	Ile	Lys	Ser	Pro	Ile	Gly	His	Ala	Leu	Gly	Gly	Lys	Gln	Tyr	Ile	225	230	235
Gln	His	Glu	Asn	Pro	Phe	Glu	Val	Gly	Met	Ser	Gly	Leu	Leu	Gly	Tyr	245	250	255
Gly	Ala	Cys	Val	Asp	Ala	Ser	Asn	Glu	Ala	Asp	Leu	Leu	Ile	Leu	Leu	260	265	270
Gly	Thr	Asp	Phe	Pro	Tyr	Ser	Asp	Phe	Leu	Pro	Lys	Asp	Asn	Val	Ala	275	280	285
Gln	Val	Asp	Ile	Asn	Gly	Ala	His	Ile	Gly	Arg	Arg	Thr	Thr	Val	Lys	290	295	300
Tyr	Pro	Val	Thr	Gly	Asp	Val	Ala	Ala	Thr	Ile	Glu	Asn	Ile	Leu	Pro	305	310	315
His	Val	Lys	Glu	Lys	Thr	Asp	Arg	Ser	Phe	Leu	Asp	Arg	Met	Leu	Lys	325	330	335
Ala	His	Glu	Arg	Lys	Leu	Ser	Ser	Val	Val	Glu	Thr	Tyr	Thr	His	Asn	340	345	350
Val	Glu	Lys	His	Val	Pro	Ile	His	Pro	Glu	Tyr	Val	Ala	Ser	Ile	Leu	355	360	365
Asn	Glu	Leu	Ala	Asp	Lys	Asp	Ala	Val	Phe	Thr	Val	Asp	Thr	Gly	Met	370	375	380
Cys	Asn	Val	Trp	His	Ala	Arg	Tyr	Ile	Glu	Asn	Pro	Glu	Gly	Thr	Arg	385	390	395
Asp	Phe	Val	Gly	Ser	Phe	Arg	His	Gly	Thr	Met	Ala	Asn	Ala	Leu	Pro	405	410	415
His	Ala	Ile	Gly	Ala	Gln	Ser	Val	Asp	Arg	Asn	Arg	Gln	Val	Ile	Ala	420	425	430
Met	Cys	Gly	Asp	Gly	Gly	Leu	Gly	Met	Leu	Leu	Gly	Glu	Leu	Leu	Thr	435	440	445
Val	Lys	Leu	His	Gln	Leu	Pro	Leu	Lys	Ala	Val	Val	Phe	Asn	Asn	Ser	450	455	460
Ser	Leu	Gly	Met	Val	Lys	Leu	Glu	Met	Leu	Val	Glu	Gly	Gln	Pro	Glu	465	470	475
Phe	Gly	Thr	Asp	His	Glu	Glu	Val	Asn	Phe	Ala	Glu	Ile	Ala	Ala	Ala			

485

490

495

Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu  
500 505 510

Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile  
515 520 525

Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu  
530 535 540

Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly  
545 550 555 560

Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile  
565 570 575

Pro Thr Pro

<210> 3

<211> 875

<212> DNA

<213> Corynebacterium glutamicum

<400> 3

tgcgagatgg	tgaatggtgg	tgagcagggt	gaacgcattt	tgcatacacgc	gattcagtc	60
accatggcgg	gtaaaggtgt	gtcggtggtg	gtgattcctg	gtgatatcgc	taaggaagac	120
gcagggtgacg	gtacttattc	caattccact	atttcctctg	gcactcctgt	gggtgtcccg	180
gatactactg	aggctgcagc	gctgggtggag	gcgattaaca	acgctaagtc	tgtaactttg	240
ttctgcggtg	cgggcgtgaa	gaatgctcgc	gcgcagggtg	tggagttggc	ggagaagatt	300
aaatcaccga	tcgggcatgc	gctgggtggt	aagcagtaca	tccagcatga	gaatccgttt	360
gaggtcggca	tgtctggcct	gcttggttac	ggcgctgcg	tggatgcgtc	caatgaggcg	420
gatctgctga	ttctattggg	tacggatttc	ccttattctg	atttccttcc	taaagacaac	480
gttgcccagg	tggatatcaa	cggtgcgac	attggtcgac	gtaccacggt	gaagtatccg	540
gtgaccggtg	atgttgctgc	aacaatcgaa	aatattttgc	ctcatgtgaa	ggaaaaaaca	600
gatcgttcct	tccttgatcg	gatgctcaag	gcacacgagc	gtaagttgag	ctcggtggtg	660
gagacgtaca	cacataacgt	cgagaagcat	gtgcctattc	accctgaata	cgttgccctc	720
atgttgaaacg	agctggcgga	taaggatgcg	gtgtttactg	tggataccgg	catgtgcaat	780
gtgtggcatg	cgaggtacat	cgagaatccg	gagggaaacgc	gcgactttgt	gggttcattc	840
cgccacggca	cgatggctaa	tgcgttgctc	catgc			875